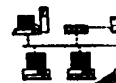


(200)

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/534376

Art Unit / Team No. :

01PE

Date Processed by STIC:

4/15/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/534,376

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/534,376

DATE: 04/15/2000

TIME: 14:27:24

Input Set: I534376.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

DS3

Does Not Comply
Corrected Diskette Needed

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2 Joukov, Vladimir
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4 AND GENE, MUTANTS THEREOF, AND USES THEREOF
5 <130> FILE REFERENCE: 28967/34140A
6 <140> CURRENT APPLICATION NUMBER: US/09/534,376
7 <141> CURRENT FILING DATE: 2000-03-24
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9 <151> EARLIER FILING DATE: 1999-11-05
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212          35              40

```

213 <210> SEQ ID NO 5

214 <211> LENGTH: 18

215 <212> TYPE: PRT

216 <213> ORGANISM: Homo sapiens

217 <220> FEATURE:

218 <223> OTHER INFORMATION: At position 1, Xaa = Unknown

219 <220> FEATURE:

```

220 <223> OTHER INFORMATION: N-terminal sequence from VEGF-C purified from PC-3
221      conditioned medium

```

222 <400> SEQUENCE: 5

W--> 223 Xaa Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile

```

224          1              5              10              15

```

225 Leu Lys

226 <210> SEQ ID NO 6

227 <211> LENGTH: 219

228 <212> TYPE: DNA

229 <213> ORGANISM: Artificial Sequence

230 <220> FEATURE:

```

231 <223> OTHER INFORMATION: Description of Artificial Sequence: vector and
232      human VEGF-C cDNA

```

233 <400> SEQUENCE: 6

```

234      tcactatagg gagaccaag cttggtaccg agctcggatc cactagtaac ggccgccagt 60
235      gtggtggaat tcgacgaact catgactgta ctctaccag aatattggaa aatgtacaag 120

```

```

236      tgtcagctaa ggcaaggagg ctggcaacat aacagagaac aggccaacct caactcaagg 180
237      acagaagaga ctataaaatt cgctgcagca cactacaac                                     219

```

238 <210> SEQ ID NO 7

239 <211> LENGTH: 1997

240 <212> TYPE: DNA

241 <213> ORGANISM: Homo sapiens

242 <220> FEATURE:

243 <221> NAME/KEY: CDS

<222> LOCATION: (352)..(1608)

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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VERIFICATION SUMMARY
PATENT APPLICATION US/09/534,376

DATE: 04/15/2000
TIME: 14:27:24

Input Set: I534376.RAW

Line	? Error/Warning	Original Text
105	W "N" or "Xaa" used: Feature required	gaaagggaga cgccctttca tggctctgctg agtaacag
223	W "N" or "Xaa" used: Feature required	Xaa Glu Glu Thr Ile Lys Phe Ala Ala Ala H
336	W Invalid/Missing Amino Acid Numbering	
1245	W "N" or "Xaa" used: Feature required	Gly Val Ala Thr Asn Thr Phe Phe Lys Pro P